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| Applicant  | : | Leivan DeVeylder et al                                | Examiner: C. Collins |
|------------|---|---|----------------------|
| Serial No. | : | 09/574,735  | •                    |
| Conf. No.  | : | 1507  | Art Unit:            |
| Filed      | : | May 18, 2000  |                      |
| For        | : | CYCLIN-DEPENDENT KINASE INHIBITORS ) AND USES THEREOF |                      |

## STATEMENT UNDER 37 C.F.R. § 1.825(a) AND (b)

Assistant Commissioner for Patents Washington, D.C. 20231

Dear Sir:

I hereby state that support for the substitute paper copy of the Sequence Listing exists in the above-captioned application as originally filed. The substitute paper copy of the Sequence Listing submitted herewith does not add new matter to the application as originally filed. In addition, the information recorded in the substitute computer readable form (CRF) of the Sequence Listing submitted herewith, is identical to the information contained in the substitute paper copy of the Sequence Listing.

Dated: August 24, 2001

Respectfully submitted,

Ann R. Pokalsky

Registration No. 34,697

Nixon Peabody LLP 990 Stewart Avenue Garden City, New York 11530-4838

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Muad. Mates

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Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

|      | 1.         | This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicar attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulema notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998). | 1114          |
|------|------------|--|---------------|
|      | 2.         | This application does not contain, as a separate part of the disclosure on paper copy, a "Sequer Listing" as required by 37 C.F.R. 1.821(c).   | nce           |
|      | 3.         | A copy of the "Sequence Listing" in computer readable form has not been submitted as required 37 C.F.R. 1.821(e).  | by            |
|      |            | A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.82 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."  | 2             |
| X    |            | The computer readable form that has been filed with this application has been found to be dama and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).  | ged           |
|      | 6.         | The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).  |               |
| П    | 7.         | Other:   |               |
|      |            |  |               |
| Αp   | plia       | cant Must Provide:   | 3             |
| X    | •          | n initial or substitute computer readable form (CRF) copy of the "Sequence Listing".   | ÷             |
| X    | An<br>into | n initial or <u>substitute</u> paper copy of the "Sequence Listing", as well as an amendment directing its of the specification.   | entry         |
| X    | ap         | statement that the content of the paper and computer readable copies are the same and, where plicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.25(b) or 1.825(d).  |               |
|      |            |  | ਜ<br>ਹ        |
| For  | qu         | uestions regarding compliance to these requirements, please contact:   | <u>.</u>      |
|      |            | ules Interpretation, call (703) 308-4216   | CENTER 1600/2 |
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| ı al |            | echnical Assistance703-287-0200  | <u>න</u>      |
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### SEQUENCE LISTING

<110> De Veylder, Lieven Beeckman, Tom Inzé, Dirk Van Camp, Wim Krols, Luc

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| ctg   | yaay   | utu a   |   |  |  |  |  | $\alpha - \alpha$                                      | aca  | $\alpha$ ++  | 200  | 202  | 2772  | ~ 2 2  | CGS   | 112                      |
|   |  | , ,   | roge  | Lyca   | yy as  | jacc   |  |  |  |  | agg<br>Arg<br>5                                      |  |   |  | cga<br>Arg  | 112                      |
| Asp<br>10   | Val  | gtt<br>Val  | gaa<br>Glu  | gag<br>Glu   | aat<br>Asn<br>15   | gga<br>Gly   | Met<br>1<br>gtt<br>Val                                   | Ala<br>acg<br>Thr                                      | Ala<br>acg<br>Thr                                      | Val<br>acg<br>Thr<br>20  | Arg<br>5<br>acg<br>Thr                               | Arg<br>gtg<br>Val  | Arg<br>aaa<br>L <u>y</u> s  | Glu<br>cga<br>Arg  | Arg<br>agg<br>Arg<br>25                             | 112<br>160               |
| Asp<br>10<br>aag  | Val  | gtt   | gaa<br>Glu<br>gag   | gag<br>Glu<br>gaa  | aat<br>Asn<br>15<br>gtg  | gga<br>Gly<br>gat  | Met<br>1<br>gtt<br>Val<br>tta                            | Ala<br>acg<br>Thr                                      | Ala<br>acg<br>Thr                                      | Val<br>acg<br>Thr<br>20<br>tct   | Arg<br>5<br>acg<br>Thr                               | Arg<br>gtg<br>Val<br>ata   | Arg<br>aaa<br>Lys<br>att  | Glu<br>cga<br>Arg<br>ctg                                   | agg<br>Arg<br>25<br>tct                             |                          |
| Asp<br>10<br>aag<br>Lys<br>ccg  | Val<br>atg<br>Met  | gtt<br>Val<br>gag   | gaa<br>Glu<br>gag<br>Glu<br>cag   | gag<br>Glu<br>gaa<br>Glu<br>30<br>gcg  | aat<br>Asn<br>15<br>gtg<br>Val   | gga<br>Gly<br>gat<br>Asp   | Met<br>1<br>gtt<br>Val<br>tta<br>Leu                     | Ala<br>acg<br>Thr<br>gtg<br>Val                        | Ala acg Thr gaa Glu 35 gga                             | Val acg Thr 20 tct Ser att   | Arg<br>5<br>acg<br>Thr<br>agg<br>Arg                 | Arg gtg Val ata Ile gcg  | Arg aaa Lys att Ile aga   | Glu<br>cga<br>Arg<br>ctg<br>Leu<br>40<br>aat               | Arg agg Arg 25 tct Ser tca                          | 160                      |
| Asp<br>10<br>aag<br>Lys<br>ccg<br>Pro   | Val<br>atg<br>Met<br>tgt<br>Cys  | gtt<br>Val<br>gag<br>Glu<br>gta                                   | gaa<br>Glu<br>gag<br>Glu<br>cag<br>Gln<br>45<br>tcg                             | gag<br>Glu<br>gaa<br>Glu<br>30<br>gcg<br>Ala   | aat<br>Asn<br>15<br>gtg<br>Val<br>acg<br>Thr   | gga<br>Gly<br>gat<br>Asp<br>aat<br>Asn   | Met 1 gtt Val tta Leu cgc Arg                            | Ala acg Thr gtg Val ggt Gly 50 gtt                     | Ala acg Thr gaa Glu 35 gga Gly ata                     | Val acg Thr 20 tct Ser att Ile   | Arg 5 acg Thr agg Arg Gtg Val                        | Arg gtg Val ata Ile gcg Ala cgg  | aaa<br>Lys<br>att<br>Ile<br>aga<br>Arg<br>55<br>cga                             | Glu<br>cga<br>Arg<br>ctg<br>Leu<br>40<br>aat<br>Asn        | Arg agg Arg 25 tct Ser tca Ser                      | 160<br>208               |
| Asp<br>10<br>aag<br>Lys<br>ccg<br>Pro<br>gca<br>Ala                                   | Val<br>atg<br>Met<br>tgt<br>Cys<br>gga<br>Gly                            | gtt<br>Val<br>gag<br>Glu<br>gta<br>Val<br>gcg<br>Ala              | gaa<br>Glu<br>gag<br>Glu<br>cag<br>Gln<br>45<br>tcg<br>Ser                      | gag<br>Glu<br>gaa<br>Glu<br>30<br>gcg<br>Ala<br>gag<br>Glu                             | aat<br>Asn<br>15<br>gtg<br>Val<br>acg<br>Thr<br>acg<br>Thr                                   | gga<br>Gly<br>gat<br>Asp<br>aat<br>Asn<br>agt<br>Ser                                   | Met 1 gtt Val tta Leu cgc Arg gtt Val 65 caa             | Ala acg Thr gtg Val ggt Gly 50 gtt Val atc             | Ala acg Thr gaa Glu 35 gga Gly ata Ile                 | Val<br>acg<br>Thr<br>20<br>tct<br>Ser<br>att<br>Ile<br>gta<br>Val<br>gaa | Arg 5 acg Thr agg Arg gtg Val cga Arg gaa            | Arg gtg Val ata Ile gcg Ala cgg Arg 70 gat                               | Arg aaa Lys att Ile aga Arg 55 cga Arg  | ctg<br>ctg<br>Leu<br>40<br>aat<br>Asn<br>gat<br>Asp        | agg<br>Arg<br>25<br>tct<br>Ser<br>tca<br>Ser<br>tct | 160<br>208<br>256        |
| Asp<br>10<br>aag<br>Lys<br>ccg<br>Pro<br>gca<br>Ala<br>cct<br>Pro<br>tcg<br>Ser<br>90 | Val<br>atg<br>Met<br>tgt<br>Cys<br>gga<br>Gly<br>ccg<br>Pro<br>75<br>tgt | gtt<br>Val<br>gag<br>Glu<br>gta<br>Val<br>gcg<br>Ala<br>60<br>gtt | gaa<br>Glu<br>gag<br>Glu<br>cag<br>Gln<br>45<br>tcg<br>Ser<br>gaa<br>Glu<br>tct | gag<br>Glu<br>gaa<br>Glu<br>30<br>gcg<br>Ala<br>gag<br>Glu<br>gaa<br>Glu<br>aca<br>Thr | aat<br>Asn<br>15<br>gtg<br>Val<br>acg<br>Thr<br>acg<br>Thr<br>cag<br>Gln<br>tcg<br>Ser<br>95 | gga<br>Gly<br>gat<br>Asp<br>aat<br>Asn<br>agt<br>Ser<br>tgt<br>Cys<br>80<br>gaa<br>Glu | Met 1 gtt Val tta Leu cgc Arg gtt Val 65 caa Gln gag Glu | Ala acg Thr gtg Val ggt Gly 50 gtt Val atc Ile aaa Lys | Ala acg Thr gaa Glu 35 gga Gly ata Ile gaa Glu tcg Ser | Val acg Thr 20 tct Ser att Ile gta Val gaa Glu aaa Lys 100               | Arg 5 acg Thr agg Arg Val cga Arg gaa Glu 85 cgg Arg | gtg<br>Val<br>ata<br>Ile<br>gcg<br>Ala<br>cgg<br>Arg<br>70<br>gat<br>Asp | aaa<br>Lys<br>att<br>Ile<br>aga<br>Arg<br>55<br>cga<br>Arg<br>tcg<br>Ser<br>atc | ctg<br>Leu<br>40<br>aat<br>Asn<br>gat<br>Asp<br>tcg<br>Ser | agg Arg 25 tct Ser tca Ser tct Yal ttt Phe 105      | 160<br>208<br>256<br>304 |

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                                                                      496
Trp Ile Tyr Asp Asp Leu Asn Lys Ser Glu Glu Ser Met Asn Met Asp
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tet tet teg gtg get gtt gaa gat gta gag tet ege ege agg tta agg
                                                                      544
Ser Ser Ser Val Ala Val Glu Asp Val Glu Ser Arg Arg Leu Arg
                            145
aag agt ctc cat gag acg gtg aag gaa gct gag tta gaa gat ttt ttt
                                                                      592
Lys Ser Leu His Glu Thr Val Lys Glu Ala Glu Leu Glu Asp Phe Phe
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cag gtg gcg gag aaa gat ctt cgg aat aag ttg ttg gaa tgt tct atg
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Gln Val Ala Glu Lys Asp Leu Arg Asn Lys Leu Leu Glu Cys Ser Met
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Ser Ala Leu Pro Asn Asp Ser Ser Cys Tyr Leu Gln Leu Arg Ser Arg
Arg Leu Glu Lys Pro Ser Ser Leu Ile Glu Pro Lys Gln Pro Pro Arg
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                                       7.5
Val His Arg Ser Gly Ile Lys Glu Ser Gly Ser Arg Ser Arg Val Asp
                                   90
Ser Val Asn Ser Val Pro Val Ala Gln Ser Ser Asn Glu Asp Glu Cys
           100
                               105
Phe Asp Asn Phe Val Ser Val Gln Val Ser Cys Gly Glu Asn Ser Leu
                           120
                                               125
Gly Phe Glu Ser Arg His Ser Thr Arg Glu Ser Thr Pro Cys Asn Phe
                       135
                                           140
Val Glu Asp Met Glu Ile Met Val Thr Pro Gly Ser Ser Thr Arg Ser
                   150
                                      155
Met Cys Arg Ala Thr Lys Glu Tyr Thr Arg Glu Gln Asp Asn Val Ile
               165
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Pro Thr Thr Ser Glu Met Glu Glu Phe Phe Ala Tyr Ala Glu Gln Gln
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Leu Lys Ser Lys Ser Glu Ser Pro Ser Pro Asn Ser Thr Pro Thr Pro
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                                                                   208
Ser Pro Ser Pro Ser Pro Thr Pro Ile Thr Thr Asn Ser Pro Pro Pro
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Thr Thr Pro Asn Ser Ser Asp Gly Val Arg Thr Arg Ala Arg Thr Leu
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Pro Glu Pro Glu Asn Ala Glu Phe Lys Glu Asn Ala Glu Asp Thr Glu
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Arg Ser Ala Arg Glu Thr Thr Pro Val His Leu Ile Met Arg Ala Asp
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Arg Thr Arg Ala Arg Thr Leu Ala Leu Glu Asn Ser Asn Asn Gln Asn
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Gln Asn Leu Ser Val Ser Ser Asp Ser Tyr Leu Gln Leu Arg Asn Arg
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120

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His Leu Ile Met Arg Ala Asp Val Leu Arg Pro Pro Arg Pro Ile Thr
                    150
                                        155
Arg Arg Thr Phe Pro Thr Glu Ala Asn Pro Lys Thr Glu Gln Pro Thr
                165
                                    170
Ile Pro Ile Ser Arg Glu Phe Glu Glu Phe Cys Ala Lys His Glu Ala
                                185
                                                    190
Glu Gln Gln Arg Glu Phe Met Glu Lys Tyr Asn Phe Asp Pro Val Thr
                            200
                                                205
Glu Gln Pro Leu Pro Gly Arg Tyr Glu Trp Glu Lys Val Ser Pro
<210> 7
<211> 25
<212> DNA
<213> Artificial Sequence
<223> Description of Artificial Sequence: Probe or
      Primer
<400> 7
                                                                   25
cgagatctga attcatggat cagta
<210> 8
<211> 26
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Probe or
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                                                                   26
cgagatctga attcctaagg catgcc
<210> 9
<211> 29
<212> DNA
<213> Artificial Sequence
<223> Description of Artificial Sequence: Probe or
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<400> 9
                                                                   29
gggaatccat gggcggcggt taggagaag
<210> 10
<211> 27
<212> DNA
<213> Artificial Sequence
<223> Description of Artificial Sequence: Probe or
      Primer
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| <400>                            | 10<br>atoco gtottottoa tggatto                      | 27 |
|----------------------------------|---|----|
| 33-33                            |   |    |
| <210><br><211><br><212><br><213> | 29  |    |
| <220>                            |   |    |
|                                  | Description of Artificial Sequence: Probe or Primer |    |
| <400>                            | 11  |    |
| ggcgaa                           | atcca tggaagtctc taaagcaac                          | 29 |
|                                  |   |    |
| <210>                            |   |    |
| <211><212>                       |   |    |
|                                  | Artificial Sequence                                 |    |
|                                  | •   |    |
| <220>                            | Description of Artificial Sequence: Probe or        |    |
| 12207                            | Primer  |    |
| <400>                            | 12  |    |
|                                  | 12<br>atcct tttgaacttc atggtttgac                   | 30 |
| 55-55-                           |   |    |
| <210>                            | 13  |    |
| <211>                            |   |    |
| <212>                            | ·   |    |
| <213>                            | Artificial Sequence                                 |    |
| <220>                            | ·   |    |
| <223>                            | Description of Artificial Sequence: Probe or Primer |    |
|                                  | LITIMET   |    |
| <400>                            |   | 26 |
| cggcto                           | cgagg agaaccacaa acacgc                             | 26 |
|                                  |   |    |
| <210><br><211>                   |   |    |
| <212>                            |   |    |
| <213>                            | Artificial Sequence                                 |    |
| <220>                            |   |    |
|                                  | Description of Artificial Sequence: Probe or        |    |
| •                                | Primer  |    |
| <400>                            | 14  |    |
|                                  | ctagt taattacctc aaggaag                            | 27 |
|                                  |   |    |
| <210>                            | 15  |    |
| <211>                            |   |    |
| <212>                            | DNA Artificial Sequence                             |    |

| <220><br><223>                   | Description of Artificial Primer    | Sequence: | Probe or |    |
|----------------------------------|-------------------------------------|-----------|----------|----|
| <400><br>gatccc                  | 15<br>egggc gatatcagcg tcatgg       |           |          | 26 |
| <210><br><211><br><212><br><213> | 25                                  |           |          |    |
| <220><br><223>                   | Description of Artificial Primer    | Sequence: | Probe or |    |
| <400><br>gatccc                  | 16<br>gggt tagtetgtta actee         |           |          | 25 |
| <210><br><211><br><212><br><213> | 24                                  |           |          |    |
| <220><br><223>                   | Description of Artificial<br>Primer | Sequence: | Probe or |    |
| <400><br>gcagct                  | 17<br>acgg agccggagaa ttgt          |           |          | 24 |
| <210><br><211><br><212><br><213> | 27                                  |           | •        |    |
|                                  | Description of Artificial Primer    | Sequence: | Probe or |    |
| <400><br>tctcct                  | 18<br>tete gaaategaaa ttgtaet       |           |          | 27 |
| <210><211><211><212><212><213>   | 26                                  |           |          |    |
|                                  | Description of Artificial<br>Primer | Sequence: | Probe or |    |
| <400><br>cggctc                  | 19<br>gagg agaaccacaa acacgc        |           |          | 26 |

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<210> 20
<211> 27
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                                                                   27
<210> 21
<211> 26
<212> DNA
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                                                                   26
<210> 22
<211> 25
<212> DNA
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<223> Description of Artificial Sequence: Probe or
      Primer
<400> 22
                                                                   25
gatcccgggt tagtctgtta actcc
<210> 23
<211> 69
<212> DNA
<213> Artificial Sequence
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<223> Description of Artificial Sequence: Probe or
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<400> 23
cccgctcgag atggtgagaa aatatagaaa agctaaagga tttgtagaag ctggagtttc 60
gtcaacgta
<210> 24
<211> 30
<212> DNA
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<220>
<223> Description of Artificial Sequence: Probe or
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| <400> 24 ggactagttc actctaactt tacccattcg                       | 30   |
|---|------|
| <210> 25<br><211> 32<br><212> DNA<br><213> Artificial Sequence  |      |
| <220> <223> Description of Artificial Sequence: Probe or Primer |      |
| <400> 25 gatcatctta agcatcatcg tcttcttcat gg                    | 32   |
| <210> 26<br><211> 19<br><212> DNA<br><213> Artificial Sequence  |      |
| <220> <223> Description of Artificial Sequence: Probe or Primer |      |
| <400> 26 taggagcata tggcggcgg                                   | 19   |
| <210> 27<br><211> 20<br><212> DNA<br><213> Artificial Sequence  |      |
| <220> <223> Description of Artificial Sequence: Probe or Primer |      |
| <400> 27<br>atatcagcgc catggaagtc                               | . 20 |
| <210> 28<br><211> 27<br><212> DNA<br><213> Artificial Sequence  |      |
| <220> <223> Description of Artificial Sequence: Probe or Primer |      |
| <400> 28 ggagctggat ccttttggaa ttcatgg                          | 27   |
| <210> 29<br><211> 19<br><212> DNA<br><213> Artificial Sequence  |      |

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       Primer
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                                                                     19
 taggagcata tggcggcgg
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 atcatcgaat tcttcatgga ttc
                                                                    23
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                                                                    20
atatcagcgc catggaagtc
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                                                                    2.7
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<210> 33
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<212> PRT
<213> Arabidopsis thaliana
<220>
<221> UNSURE
 <222> (5)
<223> Xaa at postiion 5 may be Asp or Glu
<220>
 <221> UNSURE
 <222> (6)..(8)
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<400> 33
Val Arg Arg Xaa Xaa Xaa Xaa Val Glu Glu
<210> 34
<211> 8
<212> PRT
<213> Arabidopsis thaliana
<220>
<221> UNSURE
<222> (2)..(3)
<223> Xaa at positions 2 and 3 may be any amino acid
<400> 34
Phe Xaa Xaa Lys Tyr Asn Phe Asp
<210> 35
<211> 8
<212> PRT
<213> Arabidopsis thaliana
<220>
<221> UNSURE
<222> (1)
<223> Xaa at position 1 may be Pro or Leu
<220>
<221> UNSURE
<222> (3)
<223> Xaa at position 3 may be any amino acid
<400> 35
Xaa Leu Xaa Gly Arg Tyr Glu Trp
<210> 36
<211> 10
<212> PRT
<213> Arabidopsis thaliana
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<221> UNSURE
<222> (2)
<223> Xaa at position 2 may be any amino acid
<220>
<221> UNSURE
<222> (4)
<223> Xaa at position 4 may be Asp or Glu
<220>
<221> UNSURE
<222> (7)..(9)
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<223> Xaa at positions 7, 8 or 9 may be any amino acid
<400> 36
Glu Xaa Glu Xaa Phe Phe Xaa Xaa Xaa Glu
            5
<210> 37
<211> 8
<212> PRT
<213> Arabidopsis thaliana
<220>
<221> UNSURE
<222> (2)
<223> Xaa at position 2 may be any amino acid
<400> 37 ·
Tyr Xaa Gln Leu Arg Ser Arg Arg
<210> 38
<211> 9
<212> PRT
<213> Arabidopsis thaliana
<220>
<221> UNSURE
<222> (5)
<223> Xaa at position 5 may be Met or Ile
<220>
<221> UNSURE
<222> (6)
<223> Xaa at position 6 may be Lys or Arg
<220>
<221> UNSURE
<222> (8)
<223> Xaa at position 8 may be any amino acid
<220>
<221> UNSURE
<222> (9)
<223> Xaa at position 9 may be Lys or Arg
<400> 38
Met Gly Lys Tyr Xaa Xaa Lys Xaa Xaa
                  5
<210> 39
<211> 8
<212> PRT
<213> Arabidopsis thaliana
<220>
<221> UNSURE
<222> (2)
<223> Xaa at position 2 may be any amino acid
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<400> 39 Ser Xaa Gly Val Arg Thr Arg Ala 1 5

<210> 40 <211> 327 <212> PRT <213> Arabidopsis thaliana

<400> 40

Met Gly Lys Tyr Ile Arg Lys Ser Lys Ile Asp Gly Ala Gly Ala Gly 10 Ala Gly Gly Gly Gly Gly Gly Gly Gly Glu Ser Ser Ile Ala 25 Leu Met Asp Val Val Ser Pro Ser Ser Ser Ser Leu Gly Val Leu 40 Thr Arg Ala Lys Ser Leu Ala Leu Gln Gln Gln Gln Arg Cys Leu 55 Leu Gln Lys Pro Ser Ser Pro Ser Ser Leu Pro Pro Thr Ser Ala Ser 70 75 Pro Asn Pro Pro Ser Lys Gln Lys Met Lys Lys Lys Gln Gln Met 90 Asn Asp Cys Gly Ser Tyr Leu Gln Leu Arg Ser Arg Arg Leu Gln Lys 100 105 Lys Pro Pro Ile Val Val Ile Arg Ser Thr Lys Arg Arg Lys Gln Gln 120 Arg Arg Asn Glu Thr Cys Gly Arg Asn Pro Asn Pro Arg Ser Asn Leu 135 Asp Ser Ile Arg Gly Asp Gly Ser Arg Ser Asp Ser Val Ser Glu Ser 150 Val Val Phe Gly Lys Asp Lys Asp Leu Ile Ser Glu Ile Asn Lys Asp 165 170 Pro Thr Phe Gly Gln Asn Phe Phe Asp Leu Glu Glu His Thr Gln 180 185 Ser Phe Asn Arg Thr Thr Arg Glu Ser Thr Pro Cys Ser Leu Ile Arg 200 Arg Pro Glu Ile Met Thr Thr Pro Gly Ser Ser Thr Lys Leu Asn Ile 215 220 Cys Val Ser Glu Ser Asn Gln Arg Glu Asp Ser Leu Ser Arg Ser His 230 235 Arg Arg Pro Thr Thr Pro Glu Met Asp Glu Phe Phe Ser Gly Ala 245 250 Glu Glu Glu Gln Gln Lys Gln Phe Ile Glu Lys Tyr Val Phe Pro Arg 270 265 Phe Ile Cys Ser Val Leu Leu Val Met Ser Phe Gln Phe Val Leu Phe 275 280 285 Phe Ser Phe Gly Leu Val Ser Leu Met Val Ser Val Asn Ser Phe Phe 295 300 Arg Tyr Asn Phe Asp Pro Val Asn Glu Gln Pro Leu Pro Gly Arg Phe 310 315 Glu Trp Thr Lys Val Asp Asp 325

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<400> 41
agaccatggc ggcggttagg ag
                                                                22
<210> 42
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      12
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<213> Tag·100 epitope
<400> 42
Glu Glu Thr Ala Arg Phe Gln Pro Gly Tyr Arg Ser
<210> 43
<211>
      10
<212> PRT
<213> c-myc epitope
<400> 43
Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
    . 5
<210> 44
      7
<211>
<212> PRT
<213> FLAG-epitope
<400> 44
Asp Tyr Lys Asp Asp Lys
<210> 45
<211>
<212>
      PRT
<213> HA-epitope
<400> 45
Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
<210> 46
<211> 12
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<213> protein C epitope
<400> 46
Glu Asp Gln Val Asp Pro Arg Leu Ile Asp Gly Lys
<210> 47
<211> 11
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G198628.1

<212> PRT
<213> VSV epitope

<400> 47
Tyr Thr Asp Ile Glu Met Asn Arg Leu Gly Lys
1 5 10

<210> 48
<211> 9
<212> DNA

<400> 48
agg aga aga
Arg Arg Arg